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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/721,495A

DATE: 03/18/2002
 TIME: 15:29:10

Input Set : A:\-7-2-1.app
 Output Set: N:\CRF3\03182002\I721495A.raw

3 <110> APPLICANT: Gosling, Jennifa
 4 Dairaghi, Daniel J.
 5 Hanley, Michael
 6 Miao, Zhenhua
 7 Talbot, Dale
 8 Schall, Thomas J.
 9 ChemoCentryx, Inc.
 11 <120> TITLE OF INVENTION: Chemokine Receptor
 13 <130> FILE REFERENCE: 019934-0007210US
 15 <140> CURRENT APPLICATION NUMBER: US 09/721,495A
 C--> 16 <141> CURRENT FILING DATE: 2002-03-05
 18 <150> PRIOR APPLICATION NUMBER: US 60/159,015
 19 <151> PRIOR FILING DATE: 1999-10-12
 21 <150> PRIOR APPLICATION NUMBER: US 60/159,210
 22 <151> PRIOR FILING DATE: 1999-10-13
 24 <150> PRIOR APPLICATION NUMBER: US 60/172,979
 25 <151> PRIOR FILING DATE: 1999-12-20
 27 <150> PRIOR APPLICATION NUMBER: US 60/173,388
 28 <151> PRIOR FILING DATE: 1999-12-28
 30 <150> PRIOR APPLICATION NUMBER: US 60/186,626
 31 <151> PRIOR FILING DATE: 2000-03-03
 33 <150> PRIOR APPLICATION NUMBER: US 09/686,019
 34 <151> PRIOR FILING DATE: 2000-10-10
 36 <160> NUMBER OF SEQ ID NOS: 14
 38 <170> SOFTWARE: PatentIn Ver. 2.1
 40 <210> SEQ ID NO: 1
 41 <211> LENGTH: 1147
 42 <212> TYPE: DNA
 43 <213> ORGANISM: Homo sapiens
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 46 <221> NAME/KEY: CDS
 47 <222> LOCATION: (1)..(1053)
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 55 1 5 10 15
 57 gaa atg aat ggc act tat gac tac agt caa tat gaa ctg atc tgt atc 96
 58 Glu Met Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile
 59 20 25 30
 61 aaa gaa gat gtc aga gaa ttt gca aaa gtt ttc ctc cct gta ttc ctc 144
 62 Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu

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65	aca ata gtt ttc gtc att gga ctt gca ggc aat tcc atg gta gtg gca	192		
66	Thr Ile Val Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala			
67	50	55	60	
69	att tat gcc tat tac aag aaa cag aga acc aaa aca gat gtg tac atc	240		
70	Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile			
71	65	70	75	80
73	ctg aat ttg gct gta gca gat tta ctc ctt cta ttc act ctg cct ttt	288		
74	Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Leu Phe Thr Leu Pro Phe			
75	85	90	95	
77	tgg gct gtt aat gca gtt cat ggg tgg gtt tta ggg aaa ata atg tgc	336		
78	Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys			
79	100	105	110	
81	aaa ata act tca gcc ttg tac aca cta aac ttt gtc tct gga atg cag	384		
82	Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln			
83	115	120	125	
85	ttt ctg gct tgt atc agc ata gac aga tat gtg gca gta act aaa gtc	432		
86	Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Lys Val			
87	130	135	140	
89	ccc agc caa tca gga gtg gga aaa cca tgc tgg atc atc tgt ttc tgt	480		
90	Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys			
91	145	150	155	160
93	gtc tgg atg gct gcc atc ttg ctg agc ata ccc cag ctg gtt ttt tat	528		
94	Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr			
95	165	170	175	
97	aca gta aat gac aat gct agg tgc att ccc att ttc ccc cgc tac cta	576		
98	Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu			
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101	gga aca tca atg aaa gca ttg att caa atg cta gag atc tgc att gga	624		
102	Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly			
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105	ttt gta gta ccc ttt ctt att atg ggg gtg tgc tac ttt atc aca gca	672		
106	Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala			
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110	Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys			
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113	gtt ctg ctc aca gtc gtt ata gtt ttc att gtc act caa ctg cct tat	768		
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118	Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile			
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121	acc agc tgc aac atg agc aaa cgc atg gac atc gcc atc caa gtc aca	864		
122	Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr			
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133 tat ggg tcc tgg aga aga cag aga caa agt gtg gag gag ttt cct ttt      1008
134 Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe
135                               325                               330                               335
137 gat tct gag ggt cct aca gag cca acc agt act ttt agc att taa      1053
138 Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile
139                               340                               345                               350
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158                               20                               25                               30
159 Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu
160                               35                               40                               45
161 Thr Ile Val Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala
162 50                               55                               60
163 Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile
164 65                               70                               75                               80
165 Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Leu Phe Thr Leu Pro Phe
166                               85                               90                               95
167 Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys
168                               100                              105                              110
169 Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln
170                               115                              120                              125
171 Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Lys Val
172                               130                              135                              140
173 Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys
174 145                              150                              155                              160
175 Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr
176                               165                              170                              175
177 Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu
178                               180                              185                              190
179 Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly
180                               195                              200                              205
181 Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala
182                               210                              215                              220
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184 225                              230                              235                              240
185 Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr

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186          245          250          255
187 Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile
188          260          265          270
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190          275          280          285
191 Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val
192          290          295          300
193 Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys
194 305          310          315          320
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206 <220> FEATURE:
207 <223> OTHER INFORMATION: chemokine receptor CCX CKR (variant)
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212 aaagttttcc ccctgtatt cctcacaata gttttcgtca ttggacttgc aggcaattcc 180
213 atggtagtgg caatttatgc ctattacaag aaacagagaa ccaaaacaga tgtgtacatc 240
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220 caaatgctag agatctgcat tggatttgta gtaccctttc ttattatggg ggtgtgctac 660
221 tttatcacag caaggacact catgaagatg ccaaacatta aaatatctcg acccctaaaa 720
222 gttctgctca cagtcgttat agttttcatt gtcactcaac tgccttataa cattgtcaag 780
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225 atcctttatg tttttatggg agcatctttc aaaaactacg ttatgaaaag ggccaagaaa 960
226 tatgggtcct ggagaagaca gagacaaagt gtggaggagt ttccttttga ttctgagggt 1020
227 cctacagagc caaccagtac ttttagcatt taaaggtaaa actgctctgc cttttgcttg 1080
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235 <213> ORGANISM: Artificial Sequence
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 258 <212> TYPE: PRT
 259 <213> ORGANISM: Homo sapiens
 261 <220> FEATURE:
 262 <223> OTHER INFORMATION: chemokine receptor CCR9
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 269 Phe Thr Asp Phe Tyr Cys Glu Lys Asn Asn Val Arg Gln Phe Ala Ser
 270 35 40 45
 271 His Phe Leu Pro Pro Leu Tyr Trp Leu Val Phe Ile Val Gly Ala Leu
 272 50 55 60
 273 Gly Asn Ser Leu Val Ile Leu Val Tyr Trp Tyr Cys Thr Arg Val Lys
 274 65 70 75 80
 275 Thr Met Thr Asp Met Phe Leu Leu Asn Leu Ala Ile Ala Asp Leu Leu
 276 85 90 95
 277 Phe Leu Val Thr Leu Pro Phe Trp Ala Ile Ala Ala Ala Asp Gln Trp
 278 100 105 110
 279 Lys Phe Gln Thr Phe Met Cys Lys Val Val Asn Ser Met Tyr Lys Met
 280 115 120 125
 281 Asn Phe Tyr Ser Cys Val Leu Leu Ile Met Cys Ile Ser Val Asp Arg
 282 130 135 140
 283 Tyr Ile Ala Ile Ala Gln Ala Met Arg Ala His Thr Trp Arg Glu Lys
 284 145 150 155 160
 285 Arg Leu Leu Tyr Ser Lys Met Val Cys Phe Thr Ile Trp Val Leu Ala
 286 165 170 175
 287 Ala Ala Leu Cys Ile Pro Glu Ile Leu Tyr Ser Gln Ile Lys Glu Glu
 288 180 185 190
 289 Ser Gly Ile Ala Ile Cys Thr Met Val Tyr Pro Ser Asp Glu Ser Thr
 290 195 200 205
 291 Lys Leu Lys Ser Ala Val Leu Thr Leu Lys Val Ile Leu Gly Phe Phe
 292 210 215 220
 293 Leu Pro Phe Val Val Met Ala Cys Cys Tyr Thr Ile Ile Ile His Thr
 294 225 230 235 240
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 296 245 250 255
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 298 260 265 270
 299 Ile Leu Leu Val Gln Thr Ile Asp Ala Tyr Ala Met Phe Ile Ser Asn

VERIFICATION SUMMARY

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